

FIG. 1

-54	AGCTGCGGCCCCGGTCTGCCAGCCAGACCCTTTGGAGAAGACCCCACTCCCTGTC	
1	ATGGGCCCCCGCTGCACCCCTGCACCCCTTTCTCTCCTGGTGCAGGTGACAGCGCTGGCT	60
	<u>M G P R C T L H P L S L L V Q V T A L A</u>	
61	GCGACTCTGGCCAGGGCAGGCTGCCTGCCTTCCTGCCCTGTGAGCTCCAGCCCCACGGC	120
	<u>A T L A Q</u> G R L P A F L P C E L Q P H G	
121	CTGGTGAAC TGCAACTGGCTCTTCCTGAAGTCCGTGCCCCACTTCTCGGCGGCAGCGCC	180
	L V N C N W L F L K S V P H F S A A A P	
181	CGGGCCAACTGACAGCCCTCTCCTTACTCTCCAACCGCATCCACCACTTGCACGACTCT	240
	R A N V T S L S L L S N R I H H L H D S	
241	GACTTCGTCCACCTGTCCAGCCTACGAACTCTCAACCTCAAGTGGAACTGCCCCGCGGCT	300
	D F V H L S S L R T L N L K W N C P P A	
301	GGCCTCAGCCCATGCACTTCCCCTGCCACATGACCATGAGCCCAACACCTTCCTGGCC	360
	G L S P M H F P C H M T I E P N T F L A	
361	GTGCCCCACCTGGAGGAGCTGAACCTGAGCTACAACAGCATCAGACCGTGCCTGCCCTG	420
	V P T L E E L N L S Y N S I T T V P A L	
421	CCCGACTCCCTCGTGTCCCTGTGCTGAGCCGACCAACATCCTGGTGCTAGACCCACC	480
	P D S L V S L S L S R T N I L V L D P T	
481	CACCTCACTGGCCTACATGCCCTGCGCTACCTGTACATGGATGGCAACTGCTACTACAAG	540
	H L T G L H A L R Y L Y M D G N C Y Y K	
541	AACCCCTGCCAGGGGGCGCTGGAGGTGGTGCCGGGTGCCCTCCTCGGCCTGGGCAACCTC	600
	N P C Q G A L E V V P G A L L G L G N L	
601	ACACATCTCTCACTCAAGTACAACAATCTCACGGAGGTGCCCCGAGCCTGCCCCCAGC	660
	T H L S L K Y N N L T E V P R S L P P S	
661	CTGGAGACCCTGCTGTTGTCTACAACCACATTGTCACCCCTGACGCTGAGGAOCTGGCC	720
	L E T L L L S Y N H I V T L T P E D L A	
721	AATCTGACTGCCCTGCGCGTGCTTGATGTGGGGGGGAAGTGGCGCGCTGTGACCATGCC	780
	N L T A L R V L D V G G N C R	
	Amended	(SEQ ID NO:1 1-834)
		(SEQ ID NO:2 1-260)

FIG. 2

781 CGCAACCCCTGCAGGGAGTGCCCAAAGGACCACCCCAAGCTGCACTCTGACACCTTCAGC 840
R N P C R E C P K D H P K L H S D T F S
841 CACCTGAGCCGCTCGAAGGCTGGTGTGAAAGACAGTTCTCTCTACAACCTGGACGCC 900
H L S R L E G L V L K D S S L Y N L D A
901 AGGTGGTTCGAGGCCTGGACAGGCTCCAAGTGCTGGACCTGAGTGAGAACTTCCTCTAC 960
R W F R G L D R L Q V L D L S E N F L Y
961 GACTGCATCACCAAGACCACGGCCTTCCAGGGCCTGGCCCGACTgCGcAAGCTCAACCTG 1020
D C I T K T T A F Q G L A R L R K L N L
1021 TCCTTCAATTACCACAAGAAGGTGTCCTTTGCCCACCTGCACCTGGCACCCCTCCTTTGGG 1080
S F N Y H K K V S F A H L H L A P S F G
1081 CACCTCCGGTCCCTGAAGGAGCTGGACATGCATGGCATCTTCTTCGGCTCGCTCAGTGAG 1140
H L R S L K E L D M H G I F F R S L S E
1141 ACCACGCTCCAACCTCTGGTCCAAGTGCCTATGCTCCAGACCCCTGCGCCTGCAGATGAAC 1200
T T L Q P L V Q L P M L Q T L R L Q M N
1201 TTCATTAACCAGGCCAGCTCAGCATCTTTGGGGCCTTCCCTGGCCTGCTGTACGTGGAC 1260
F I N Q A Q L S I F G A F P G L L Y V D
1261 CTATCGGACAACCGCATCAGCGGAGCTGCAAGGCCAGTGGcCATTACTAGGGAGGTGGAT 1320
L S D N R I S G A A R P V A I T R E V D
1321 GGTAGGGAGAGGGTCTGGCTGCCTTCCAGGAACCTCGCTCCACGTCCACTGGACACTCTC 1380
G R E R V W L P S R N L A P R P L D T L
1381 CGCTCAGAGGACTTCAIGCCAACTGCAAGGCCTTCAGCTTCACCTTGGACCTGTCTCGG 1440
R S E D F M P N C K A F S F T L D L S R
1441 AACAACTGGTGACAATCCAGTCGGAGATGTTTGCTCGCCTCTCAGCCTCGAGTGCCTG 1500
N N L V T I Q S E M F A R L S R L E C L
1501 CGTCTGAGCCACAACAGCATCTCCCAGGCGGTCAATGGCTCTCAGTTTGTGCCGCTGACC 1560
R L S H N S I S Q A V N G S O F V P L T
(SEQ ID NO:1 835-1614)
(SEQ ID NO:2 261-520)

FIG. 3

1561 AGCCTGCGGGTGCTGGACCTGTCCCACAACAAGCTGGACCTGTATCACGGGCGCTCGTTC 1620
S L R V L D L S H N K L D L Y H G R S F
1621 ACGGAGCTGCCCGCGCTGGAAGCACTGGACCTCAGCTACAACAGCCAGCCCTTTACCATG 1680
T E L P R L E A L D L S Y N S Q P F T M
1681 CAGGGTGTGGGCCACAACCTCAGCTTCGTGGCCCAGCTGCCCGCCCTGCGCTACCTCAGC 1740
Q G V G H N L S F V A Q L P A L R Y L S
1741 CTGGCGCACAATGACATCCATAGCCGAGTGTCCCAGCAGCTCTGTAGCCCTCACTGTGC 1800
L A H N D I H S R V S Q Q L C S A S L C
1801 GCCCTGGACTTTAGCGGCAACGATCTGAGCCGGATGTGGGCTGAGGGAGACCTCTATCTC 1860
A L D F S G N D L S R M W A E G D L Y L
1861 CCCTTCTTCCAAGGCCCTAAGAAGCCTAGTCTGGCTGGACCTGTCCCAGAACCACCTGCAC 1920
R F F Q G L R S L V W L D L S Q N H L H
1921 ACCCTCCTGCCACGTGCCCTGGACAACCTCCCCAAAAGCCTGAAGCATCTGCATCTCCGT 1980
T L L P R A L D N L P K S L K H L H L R
1981 GACAATAACCTGGCCTTCTTCAACTGGAGCAGCCTGACCTCCTGCCCAAGCTGGAAACC 2040
D N N L A F F N W S S L T L L P K L E T
2041 CTGGACTTGGCTGGAAACCAGCTGAAGGCCCTAAGCAATGGCAGCCTGCCATCTGGCACC 2100
L D L A G N Q L K A L S N G S L P S G T
2101 CAGCTGCGGAGGCTGGACCTCAGTGGCAACAGCATCGGCTTTGTGAACCCTGGCTTCTTT 2160
Q L R R L D L S G N S I G F V N P G F F
2161 GCCCTGGCCAAGCAGTTAGAAGAGCTCAACCTCAGCGCCAATGCCCTCAAGACAGTGGAG 2220
A L A K Q L E E L N L S A N A L K T V E
2221 CCTCCTGGTTTGGCTCGATGGTGGGCAACCTGAAAGTCCTAGACGTGAGCGCCAACCCT 2280
P S W F G S M V G N L K V L D V S A N P
2281 CTGCACTGCGCCTGTGGGGCGACCTTCGTGGGCTTCCTGCTGGAGGTACAGCCTGCGGTG 2340
L H C A C G A T F V G F L L E V Q A A V

(SEQ ID NO:1 1615-2394)

Amended

(SEQ ID NO:2 521-780)

FIG. 4

2341 CCTGGGCTGCCCAGCCGGTCAAGTGTGGCAGTCCGGGGCAGCTCCAGGGCCATAGCATC 2400
P G L P S R V K C G S P G Q L Q G H S I
2401 TTGCGCAAGACCTGCGCCTCTGOCTGGATGAGACCCTCTCGTGGAAGTGTTTTGGCATC 2460
F A Q D L R L C L D E T L S W N C F G I
2461 TCGCTGCTGGCCATGGGOCCTGGGOCCTGGTTGTGOCATGCTGCACCACCTCTGCGGCTGG 2520
S L L A M A L G L V V P M L H H L C G W
2521 GACCTCTGGTACTGCTTCCACCTGTGOCCTGGCCTGGCTGCCCCACCGAGCGCAGCGGCGG 2580
D L W Y C F H L C L A W L P H R G Q R R
2581 GGCGCAGACGCCCTGTTCTATGATGCCTTCGTGGTCTTTGACAAAGCTCAGAGTGCTGTG 2640
G A D A L F Y D A F V V F D K A Q S A V
2641 GCCGACTGGGTGTACAACGAGCTGCGGGTGCAGCTGGAGGAGCGCCGTGGGCGOCgCGCA 2700
A D W V Y N E L R V Q L E E R R G R R A
2701 CTGCGCCTGTGOCCTGGAGGAGCGAGACTGGTTACCTGGCAAGACGCTCTTCGAGAACCTG 2760
L R L C L E E R D W L P G K T L F E N L
2761 TGGGCCTCAGTCTACAGCAGCCGCAAGACCCTGTTTGTGCTGGCCCACACGGACCGTGTC 2820
W A S V Y S S R K T L F V L A H T D R V
2821 AGCGGCCTCTTGCGTGCCAGTTTCCTGCTGGCCCAGCAGCGCCTGCTGGAGGACCGCAAG 2880
S G L L R A S F L L A Q Q R L L E D R K
2881 GACGTTGTAGTGCTGGIGATCCTGCGCCCCGATGCCTACCGCTCCCGCTACGTGCGGCTG 2940
D V V V L V I L R P D A Y R S R Y V R L
2941 CGCCAgCGCCTCTGCGGCCAGAGTGTCTCCTCTGGCCCCACCAGCCCCGTGGGCAGGGC 3000
R Q R L C R Q S V L L W P H Q P R G Q G
3001 AGCTTCTGGGCCCAGCTGGGCACAGCCCTGACCAGGGACAACCGCCACTTCTATAACCGG 3060
S F W A Q L G T A L T R D N R H F Y N R
3061 AACTTCTGCCGGGGCCCCACGACAGCCGAATAG 3093 (SEQ ID NO:1 2395-3147)
N F C R G P T T A E * (SEQ ID NO:2 781-1030)

Amended

FIG. 6

SWINE	1	MGPRCT--LHPLSLLVQVTLAATLAQGRIPAFLPCELPQHGLVNCNWLFLKSVPHFSAA	58	SWINE
HUMAN	1	MGE-CRSALHPLSLLVQAIMLAMILALGTLPAFLPCELPQHGLVNCNWLFLKSVPHFSMA	59	HUMAN
MOUSE	1	MVLRRRT-LHPLSLLVQAAVLAETLALGTLPAFLPCELPQHGLVDCNWLFLKSVPHFSAA	59	MOUSE
CAT	1	MGP-CHGALHPLSLLVQAAALAVALAQGITLPAFLPCELPQHGLVNCNWLFLKSVPHFSAA	59	CAT
* . . . ***** . ** . ** . ***** . **** . ***** . ** . *				
SWINE	59	APRANVTSLSLLSNRIHHLHDSDFVHLSSLRTINLKNWCPPAGLSPMHFPCHMTIEPNTF	118	SWINE
HUMAN	60	APRGWTSLSLSSNRIHHLHDSDFAHLP SLRHLNKNWCPPVGLSPMHFPCHMTIEPSTF	119	HUMAN
MOUSE	60	ASCNITRSLSLISNRIHHLHNSDFVHLNLRQLNKNWCPPTGLSPHFSCHMTIEPRTF	119	MOUSE
CAT	60	APRGWTSLSLYSNRIHHLHDSDFVHLSSLRRLNKNWCPPASLSPMHFPCHMTIEPHTF	119	CAT
* . . * . * . *** ***** . *** . ** . ** ***** . *** . ** . ***** . **				
SWINE	119	LAVPTLEEINLSYNSITTVPALPDSLVSLSLRTINILVDPTHLTGLHALRYLYMDGNCY	178	SWINE
HUMAN	120	LAVPTLEEINLSYNNITIVPALPKSLISLSLSHTNIMLDSASLAGLHALRFLFMDGNCY	179	HUMAN
MOUSE	120	LAMPTLEEINLSYNGITTVPRLPSSLVNLSLSHTINILVDANSIAGLYSLRVLFMDGNCY	179	MOUSE
CAT	120	LAVPTLEEINLSYNSITTVPALPSSLVLSLSLRTINILVDPANLAGLSLRFIFDGNKY	179	CAT
** . . ***** * . *** . ** . ** . ***** . ** . * . ** . ** . *****				
SWINE	179	YKNPCQGALEVVPGALLGLGNLTHLSLKYNNTLTVPRSLPPSLETLLLSYNHIVTLIPED	238	SWINE
HUMAN	180	YKNPCQGALEVAPGALLGLGNLTHLSLKYNNTLTVPRNLPSSLEYLLLSYNRIVKLAPED	239	HUMAN
MOUSE	180	YKNPCTGAVKVTPGALLGLGNLTHLSLKYNNTLTKVPRQLPPSLEYLLVSYNLIVKLGPED	239	MOUSE
CAT	180	YKNPCQALQVAPGALLGLGNLTHLSLKYNNTLTVPRGLPPSLEYLLLSYNHITLAPED	239	CAT
***** * . * ***** . ***** ***** *** ** . *** . ** . *** * . * ***				
SWINE	239	LANLTALRVLDVGGNCRRCDHARNPCRECPKDHPLHSDTFSHLSRLEGVLKDSSLYNL	298	
		Amended	(SEQ ID NO:2 1-298)	
HUMAN	240	LANLTALRVLDVGGNCRRCDHAPNPMCECPRHFPQLHPDTFSHLSRLEGVLKDSSLYNL	299	
			(SEQ ID NO:4 1-299)	
MOUSE	240	LANLTSRVLDVGGNCRRCDHAPNPMCECGQKSLHLPETPHLSHLEGVLKDSSLYNL	299	
			(SEQ ID NO:6 1-299)	
CAT	240	LANLTALRVLDVGGNCRRCDHARNPMCECPKGFPHLPDTFSHLNHLLEGVLKDSSLYNL	299	
		***** . ***** ***** *** ** . . ** . ** . ***** . *	(SEQ ID NO:8 1-299)	

FIG. 7

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SWINE 299 DARWFRGLDRLQVLDLSENFYDCITKTTAFQGLARLRKINLSFNYHKKVSFAHLHLAPS 358
HUMAN 300 NASWFRGLGNLRVLDLSENFYKCTTKTKAFQGLTQLRKINLSFNYQKRVSEFAHLSLAPS 359
MOUSE 300 NSSWFQGLVNLVLDLSENFYIESINHINAFQNLTRLRKINLSFNYRKKVSEFARLHLASS 359
CAT 300 NPRWFHALGNLMVLDLSENFYDCITKTTAFQGLAQLRRINLSFNYHKKVSFAHLHLAPS 359
      . ** * * ***** * .. * *** * ** ***** * ***** * .. *
SWINE 359 FGHIRSLKELDMHGIFFRSLSETTLQPLVQLPMLQTLRLQMFINQAQLSIFGAFFPGLLY 418
HUMAN 360 FGSLVALKELDMHGIFFRSLDETTLRPLARLPLQTLRLQMFINQAQLGIFRAFFPGLRY 419
MOUSE 360 FKNLVSLQELMNGIFFRSLNKYTLRWLADLPKLHTLHLQMFINQAQLSIFGTFRALRF 419
CAT 360 FGSLLSLQQLDMHGIFFRSLSETTLRSIVHLPLQLSLHLQMFINQAQLSIFGAFFPGLRY 419
      * . * . * . ***** ..** * *** ..* ***** ..* . * . * .
SWINE 419 VDLSDNRISGAARPVAITREVDGR-ERVWLPSRNLAAPRLDTLRSEDFMPNCKAFSFTLD 477
HUMAN 420 VDLSDNRISGASELTATMGADGG-EKVVLPQGLAPAPVDTPSSEDFRPNCSLTNFTLD 478
MOUSE 420 VDLSDNRISGPSTLSEATPEEADDAEQEELLSADPHAPLSTPASKNFMDRCKNFKFTMD 479
CAT 420 VDLSDNRISGAMELAAATGEVDGG-ERVRLPSCDLALGPPGTPSSEGFMFGCKTLNFTLD 478
      ***** . . . . * .. * . * . . . . * * . * . * . * . *
SWINE 478 LSRNNLVTIQSEMFARLSRLECLRLSHNSISQAVNGSQFVPLTSLRVLDLSHNKLDLYHG 537
HUMAN 479 LSRNNLVTIQPEMFAQLSHLQCLRLSHNCISQAVNGSQFVPLTGLQVLDLSRNKLDLYHE 538
MOUSE 480 LSRNNLVTIKPEMFVNLRLQCLSLSHNSIAQAVNGSQFVPLTINLQVLDLSHNKLDLYHW 539
CAT 479 LSRNNLVTIQPEMFARLSRLOCLLSRNSISQAVNGSQFMPLTSLQVLDLSHNKLDLYHG 538
      ***** ... *** * * * * * * ***** * * * ***** *****

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Amended (SEQ ID NO:2 299-537)

(SEQ ID NO:4 300-538)

(SEQ ID NO:6 300-539)

(SEQ ID NO:8 300-538)

FIG. 8

[illegible]

FIG. 9

SWINE	838	CGNDLWYCFHLCLAWLPHRGQRRGAD--ALFYDAFVVEDKAQSAVADWVYNELRVQLEER	895
HUMAN	839	CGNDLWYCFHLCLAWLPWRGRQSGRDEDALPYDAFVVEDKTQSAVADWVYNELRGQLEEC	898
MOUSE	840	CGNDVWYCFHLCLAWLPLIARSRRSAQA-LPYDAFVVEDKAQSAVADWVYNELRVRLGR	898
CAT	839	CGNDLWYCFHLCLAWLPRRGRRRGAD---ALPYDAFVVEDKAQSAVADWVYNELRVRLGR	896
****, ***** * ***** ***** **..			
SWINE	896	RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKTLFVLAHTDRVSGLLRASFIQAQRL	955
HUMAN	899	RGRWALRLCLEERDWLPGKTLFENLWASVYGSRKTLFVLAHTDRVSGLLRASFIQAQRL	958
MOUSE	899	RGRRALRLCLEERDWLPGQTLFENLWASTYGSRKTLFVLAHTDRVSGLLRASFIQAQRL	958
CAT	897	RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKMLFVLAHTDRVSGLLRASFIQAQRL	956
, **, *****, ***** * ***, ***** *****			
SWINE	956	LEDKDVVVLVILRPDAYRSRYVRLRQRLCRQSVLLWPHQPGQGSFWAQLGTALTRDNR	1015
HUMAN	959	LEDKDVVVLVILSPDGRSRYVRLRQRLCRQSVLLWPHQPSGQSFQAQLGMALTRDNH	1018
MOUSE	959	LEDKDVVVLVILRPDAHRSRYVRLRQRLCRQSVLFWPQPNQGGFWAQLSTALTRDNR	1018
CAT	957	LEDKDVVVLVILRPDAHRSRYVRLRQRLCRQSVLLWPHQPSGQSFQAQLGTALTRDNQ	1016
***** ** ***** ***** ** ** ** ***** .. *****			
SWINE	1016	HEYNRNFCRCPTTAE (SEQ ID NO:2 838-1030)	1030
HUMAN	1019	HEYNRNFCRCPTTAE (SEQ ID NO:4 839-1032)	1032
MOUSE	1019	HEYNRNFCRCPTTAE (SEQ ID NO:6 840-1032)	1032
CAT	1017	HEYNRNFCRCPTTAE (SEQ ID NO:8 839-1031)	1031
**** * * * * *			